

SEARCH REQUEST FORM

A 57

Requestor's

Name:

S. Ungar

Serial

Number: 08/848,439

Date:

7/6/98

Phone: 305-2181

Art Unit: 1642

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

SEQ ID #2

SEQ ID #3

Please compare SEQ ID #1 to revise transcribed

SEQ ID #2

Please compare Seq ID #1 to revise transcribed

SEQ ID #3

Thanks
Susan Go

1998 JUL -7 AM 8:37

STAFF USE ONLY

Date completed: 7-10-98

Searcher: mack

Terminal time: 10

Elapsed time: 1

CPU time:

Total time: 15

Number of Searches: 1

Number of Databases: 1

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG EG

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other

> O < IntelliGenetics
> O <
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-08-848-439-1.res made by spencer on Fri Jul 10 Jul 98 15:04:54-PDT.

Query sequence being compared: US-08-848-439-1 (1-2027)
Number of sequences searched: 2
Number of scores above cutoff: 2

Results of the initial comparison of US-08-848-439-1 (1-2027) with:
File : translate.seq

100-
N -
U -
M -
B -
E -
R -
O -
F -
S -
E -
Q -
U -
N -
C -
S -
Z -
S -
SCORE 0 79 158 238 317 396 475 555 634 713
SIDEV -9 -8 -7 -6 -5 -4 -3 -2 -1 0

PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 1.00 Window size 32
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
 682 653 43.13
Times: CPU Total Elapsed
 00:00:00.00 00:00:00.00

Number of residues: 1710
Number of sequences searched: 2
Number of scores above cutoff: 2

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Score	Sig.	Frame
1. US-08-848-439-2	Sequence 2, Application US	885	713	734	0.72	0	
2. US-08-848-439-3	Sequence 3, Application US	825	652	688	-0.70	0	

1. US-08-848-439-2 (1-2027)
US-08-848-439-2 Sequence 2, Application US/08848439

Sequence 2, Application US/08848439
GENERAL INFORMATION:

APPLICANT: LAVALLE, EDWARD
TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CAMBRIDGE PARK DRIVE
CITY: CAMBRIDGE
STATE: MA
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,439
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R.

REGISTRATION NUMBER: 32,618

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 295 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

Reverse translation from the peptide US-08-848-439-2.

Note: the original peptide US-08-848-439-2 contained at least one of the residues Arg, Ile, Leu, or Ser. The nucleic acid sequence thus contains ambiguous bases which may translate into amino acids other than the original amino acids.

Initial Score = 713 Optimized score = 734 Significance = 0.72
Residue Identity = 588 Matches = 734 Mismatches = 151
Gaps = 0 Conservative Substitutions = 0

210 220 230 240 250 260 270
GCCCTCCCGCGCTCCCTCTGCCCCCTCGGGGCGGCCACGATGCGAGGCGCTGCTGC
ATGTYNCARGGNCNGNSNY
X 10 20

280 290 300 310 320 330 340
TGCCTGCTCTCTCCCTCGCGCTGCGACTGCTCCGCGGCGCGGCGCTCTCTTGTGGCCAGCCG
GNTNTNTNTTNTTTCGNCNSNCATGTYGTGTYTNGGWSGNCNGGNTTNTTNTTNGNCARCNG
30 40 50 60 70 80 90

350 360 370 380 390 400 410 420
ACTTCTCTTACAGCGCAATTCAGAGCCCATCCGCGCACCTCGAGCTGTGCCAGCGCATGATAC
ATTYMSNTAYARNGNSNAATGYARCCNATNCGCAATYTCARNTGTGCAVGGNATNGARTAC
100 110 120 130 140 150 160

[illegible]